

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/530, 696  
Source: IFWP  
Date Processed by STIC: 08/04/2006

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 08/04/2006

PATENT APPLICATION: US/10/530,696

TIME: 13:10:42

Input Set : A:\14875-141US1sq.txt

Output Set: N:\CRF4\08042006\J530696.raw

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3 <110> APPLICANT: OZAKI Shuji
4   ABE Masahiro
6 <120> TITLE OF INVENTION: Cell Death-Inducing Agent
8 <130> FILE REFERENCE: 14875-141US1
10 <140> CURRENT APPLICATION NUMBER: US 10/530,696
11 <141> CURRENT FILING DATE: 2005-04-08
13 <150> PRIOR APPLICATION NUMBER: PCT/JP03/13063
14 <151> PRIOR FILING DATE: 2003-10-10
16 <150> PRIOR APPLICATION NUMBER: JP 2002-299289
17 <151> PRIOR FILING DATE: 2002-10-11
19 <160> NUMBER OF SEQ ID NOS: 14
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 547
25 <212> TYPE: DNA
26 <213> ORGANISM: Mus musculus
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (103)..(546)
32 <400> SEQUENCE: 1
33 tacgactcac tatagggcaa gcagtggat caacgcagag tacgcgggga atctatgatc 60
35 agtgtcctct ctacacagtc cctgacgaca ctgactccaa cc atg cga tgg agc 114
36                                     Met Arg Trp Ser
37                                     1
39 tgg atc ttt ctc ttc ctc ctg tca ata act gca ggt gtc cat tgc cag 162
40 Trp Ile Phe Leu Phe Leu Leu Ser Ile Thr Ala Gly Val His Cys Gln
41   5                               10                               15                               20
43 gtc cag ttg cag cag tct gga cct gag ctg gtg aag cct ggg gct tca 210
44 Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
45                               25                               30                               35
47 gtg aag atg tct tgt aag gct tct ggc tac acc ttc aca gac tac ttt 258
48 Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Phe
49                               40                               45                               50
51 ata cac tgg gtg aaa cag agg cct gga cag gga ctt gaa tgg att gga 306
52 Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
53   55                               60                               65
55 tgg att ttt cct gga gat gat act act gat tac aat gag aag ttc agg 354
56 Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn Glu Lys Phe Arg
57   70                               75                               80
59 ggc aag acc aca ctg act gca gac aaa tcc tcc agc aca gcc tac att 402
60 Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Ile
61   85                               90                               95                               100
63 ttg ctc agc agc ctg acc tct gag gac tct gcg atg tat ttc tgt gta 450

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64 Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met Tyr Phe Cys Val
65          105          110          115
67 agg agt gac gac ttt gac tac tgg ggc cag ggc acc act ctc aca gtc 498
68 Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
69          120          125          130
71 tcc tca gcc aaa aca aca ccc cca tca gtc tat cca ctg gcc cct gct g 547
72 Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Ala
73          135          140          145
76 <210> SEQ ID NO: 2
77 <211> LENGTH: 148
78 <212> TYPE: PRT
79 <213> ORGANISM: Mus musculus
81 <400> SEQUENCE: 2
82 Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Ile Thr Ala Gly
83 1          5          10          15
85 Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
86          20          25          30
88 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
89          35          40          45
91 Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
92          50          55          60
94 Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn
95 65          70          75          80
97 Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser
98          85          90          95
100 Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met
101          100          105          110
103 Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr
104          115          120          125
106 Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro
107          130          135          140
109 Leu Ala Pro Ala
110 145
113 <210> SEQ ID NO: 3
114 <211> LENGTH: 535
115 <212> TYPE: DNA
116 <213> ORGANISM: Mus musculus
118 <220> FEATURE:
119 <221> NAME/KEY: CDS
120 <222> LOCATION: (103)..(534)
122 <400> SEQUENCE: 3
123 ctaatacgac tcactatagg gcaagcagtg gtatcaacgc agagtacgcg gggactwatg 60
125 agaatagcag taattagcta gggacccaaaa ttcaaagaca aa atg cat ttt caa 114
126          Met His Phe Gln
127          1
129 gtg cag att ttc agc ttc ctg cta atc agt gcc tca gtc atc atg tcc 162
130 Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser Val Ile Met Ser
131 5          10          15          20
133 aga gga caa att gtt ctc acc cag tcg cca gca atc atg tct gca tct 210

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134 Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser
135          25          30          35
137 cca ggg gag aag gtc acc ata acc tgc agt gcc agc tca agt gta agt 258
138 Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser
139          40          45          50
141 tac atg cac tgg ttc cag cag aag cca ggc act ttt ccc aaa ctc tgg 306
142 Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro Lys Leu Trp
143          55          60          65
145 att tat agc aca tcc aac ctg gct tct gga gtc cct act cgc ttc agt 354
146 Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Thr Arg Phe Ser
147          70          75          80
149 ggc agt gga tct ggg acc tct tac tct ctc aca atc agc cga atg gag 402
150 Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu
151 85          90          95          100
153 gct gaa gat gct gcc act tat tac tgc cag caa agg acg agt tat cca 450
154 Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Thr Ser Tyr Pro
155          105          110          115
157 ccc acg ttc ggc tcg ggg aca aag ttg gag ata aaa cgg gct gat gct 498
158 Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala
159          120          125          130
161 gca cca act gta tcc atc ttc cca cca tcc agt gag c 535
162 Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
163          135          140
166 <210> SEQ ID NO: 4
167 <211> LENGTH: 144
168 <212> TYPE: PRT
169 <213> ORGANISM: Mus musculus
171 <400> SEQUENCE: 4
172 Met His Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
173 1          5          10          15
175 Val Ile Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile
176          20          25          30
178 Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser
179          35          40          45
181 Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe
182          50          55          60
184 Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
185 65          70          75          80
187 Thr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
188          85          90          95
190 Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg
191          100          105          110
193 Thr Ser Tyr Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
194          115          120          125
196 Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
197          130          135          140
200 <210> SEQ ID NO: 5
201 <211> LENGTH: 789
202 <212> TYPE: DNA

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Input Set : A:\14875-141US1sq.txt

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203 <213> ORGANISM: Artificial Sequence

205 <220> FEATURE:

206 <223> OTHER INFORMATION: Description of Artificial Sequence:an  
artificially

207 synthesized DNA sequence

209 <220> FEATURE:

210 <221> NAME/KEY: CDS

211 <222> LOCATION: (14)..(775)

214 <400> SEQUENCE: 5

215 cctgaattcc acc atg cga tgg agc tgg atc ttt ctc ttc ctc ctg tca 49

216 Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser

217 1 5 10

219 ata act gca ggt gtc cat tgc cag gtc cag ttg cag cag tct gga cct 97

220 Ile Thr Ala Gly Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro

221 15 20 25

223 gag ctg gtg aag cct ggg gct tca gtg aag atg tct tgt aag gct tct 145

224 Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser

225 30 35 40

227 ggc tac acc ttc aca gac tac ttt ata cac tgg gtg aaa cag agg cct 193

228 Gly Tyr Thr Phe Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro

229 45 50 55 60

231 gga cag gga ctt gaa tgg att gga tgg att ttt cct gga gat gat act 241

232 Gly Gln Gly Leu Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr

233 65 70 75

235 act gat tac aat gag aag ttc agg ggc aag acc aca ctg act gca gac 289

236 Thr Asp Tyr Asn Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp

237 80 85 90

239 aaa tcc tcc agc aca gcc tac att ttg ctc agc agc ctg acc tct gag 337

240 Lys Ser Ser Ser Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu

241 95 100 105

243 gac tct gcg atg tat ttc tgt gta agg agt gac gac ttt gac tac tgg 385

244 Asp Ser Ala Met Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp

245 110 115 120

247 ggc cag ggc acc act ctc aca gtc tcc tca ggt gga ggc ggt agc caa 433

248 Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gln

249 125 130 135 140

251 att gtt ctc acc cag tcg cca gca atc atg tct gca tct cca ggg gag 481

252 Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu

253 145 150 155

255 aag gtc acc ata acc tgc agt gcc agc tca agt gta agt tac atg cac 529

256 Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His

257 160 165 170

259 tgg ttc cag cag aag cca ggc act ttt ccc aaa ctc tgg att tat agc 577

260 Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro Lys Leu Trp Ile Tyr Ser

261 175 180 185

263 aca tcc aac ctg gct tct gga gtc cct act cgc ttc agt ggc agt gga 625

264 Thr Ser Asn Leu Ala Ser Gly Val Pro Thr Arg Phe Ser Gly Ser Gly

265 190 195 200

267 tct ggg acc tct tac tct ctc aca atc agc cga atg gag gct gaa gat 673

268 Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu Asp

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269 205                210                215                220
271 gct gcc act tat tac tgc cag caa agg acg agt tat cca ccc acg ttc      721
272 Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Thr Ser Tyr Pro Pro Thr Phe
273                225                230                235
275 ggc tcg ggg aca aag ttg gag ata aaa gac tac aag gat gac gac gat      769
276 Gly Ser Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp
277                240                245                250
279 aag tga taagcggccg caat      789
280 Lys
283 <210> SEQ ID NO: 6
284 <211> LENGTH: 253
285 <212> TYPE: PRT
286 <213> ORGANISM: Artificial Sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: Description of Artificial Sequence:an
artificially
290      synthesized peptide sequence
292 <400> SEQUENCE: 6
293 Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Ile Thr Ala Gly
294   1           5           10           15
295 Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
296           20           25           30
297 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
298           35           40           45
299 Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
300           50           55           60
301 Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn
302   65           70           75           80
303 Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser
304           85           90           95
305 Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met
306           100          105          110
307 Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr
308           115          120          125
309 Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Ile Val Leu Thr
310           130          135          140
311 Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile
312 145           150          155          160
313 Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln
314           165          170          175
315 Lys Pro Gly Thr Phe Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu
316           180          185          190
317 Ala Ser Gly Val Pro Thr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser
318           195          200          205
319 Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr
320           210          215          220
321 Tyr Cys Gln Gln Arg Thr Ser Tyr Pro Pro Thr Phe Gly Ser Gly Thr
322 225           230          235          240
323 Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Lys
324           245          250

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/530,696

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Input Set : A:\14875-141US1sq.txt

Output Set: N:\CRF4\08042006\J530696.raw